

N. Kodom, D.

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/090,672B

DATE: 03/22/2000
TIME: 23:32:11

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This Raw Listing contains the General
Information Section and up to the first 5 pages.

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SEQUENCE LISTING

1
2
3 (1) General Information:
4 (i) APPLICANT: Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
5 Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
6 Shigemasa; Takei, Masami
7 (ii) TITLE OF INVENTION: IgA Nephropathy-Related Genes
8 (iii) NUMBER OF SEQUENCES: 111
9 (iv) CORRESPONDENCE ADDRESS:
10 (A) ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
11 (B) STREET: 30 Rockefeller Plaza
12 (C) CITY: New York
13 (D) STATE: New York
14 (E) ZIP: 10112-3801
15 (v) COMPUTER READABLE FORM:
16 (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
17 (B) COMPUTER: Compaq PC
18 (C) OPERATING SYSTEM: Windows 95
19 (D) SOFTWARE: WordPerfect 8.0
20 (vi) CURRENT APPLICATION DATA:
21 (A) APPLICATION NUMBER: 09/090,672
22 (B) FILING DATE: 04-JUNE-1998
23 (C) CLASSIFICATION: 435
24 (vii) PRIOR APPLICATION DATA:
25 (A) APPLICATION NUMBER: PCT/JP97/04468
26 (B) FILING DATE: 05-DEC-1997
27 (A) APPLICATION NUMBER: JP-8-325763
28 (B) FILING DATE: 05-DEC-1996
29 (viii) ATTORNEY/AGENT INFORMATION:
30 (A) NAME: Perry, Lawrence S.
31 (B) REGISTRATION NUMBER: 31865
32 (C) REFERENCE/DOCKET NUMBER: 766.21
33 (ix) TELECOMMUNICATION INFORMATION:
34 (A) TELEPHONE: (212) 218-2100
35 (B) TELEFAX: (212) 218-2200
36
37 (2) INFORMATION FOR SEQ ID NO:1:
38 (i) SEQUENCE CHARACTERISTICS:
39 (A) LENGTH: 4276 base pairs
40 (B) TYPE: nucleic acid
41 (C) STRANDEDNESS: double
42 (D) TOPOLOGY: linear
43 (ii) MOLECULE TYPE: cDNA
44 (vi) ORIGINAL SOURCE:
45 (A) ORGANISM: human
46 (G) CELL TYPE: leukocyte

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RAW SEQUENCE LISTING
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TIME: 23:32:11

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47 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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 52 Asp Gly Phe Leu Asp Asp Gly Arg Gly Asp Gln Pro Leu His Ser Gly
 53 5 10 15
 54 CTG GGT TCA CCT CAC TGC TTC AGT CAC CAG AAT GGG GAG AGA GTG GAA 154
 55 Leu Gly Ser Pro His Cys Phe Ser His Gln Asn Gly Glu Arg Val Glu
 56 20 25 30
 57 CGA TAT TCT CGA AAG GTG TTT GTA GGC GGA TTG CCT CCA GAC ATT GAT 202
 58 Arg Tyr Ser Arg Lys Val Phe Val Gly Gly Leu Pro Pro Asp Ile Asp
 59 35 40 45 50
 60 GAA GAT GAG ATC ACA GCT AGT TTT CGT CGC TTT GGC CCT CTG ATT GTG 250
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 69 GAT GCA TGC ATT GAA GAA GAT GGA AAA CTC TAC CTT TGT GTA TCA AGT 394
 70 Asp Ala Cys Ile Glu Glu Asp Gly Lys Leu Tyr Leu Cys Val Ser Ser
 71 100 105 110
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 75 GAC AGT GAC TTT GTG ATG GAT GGT TCA CAG CCA CTT GAC CCA CGA AAA 490
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 83 165 170 175
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 88 Phe Ser Asn Gln Gln Ser Tyr Ile Ala Ala Ile Ser Ala Arg Phe Val
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 90 CAG CTG CAG CAT GGA GAG ATA GAT AAA CGG GTA AGC CTT ATA CTA CAT 730
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 92 215 220 225
 93 TTT GGA AAA TTC TAGAAATGGT CCTCTAAATG TGTGATTACC AATATTAGAA 782
 94 Phe Gly Lys Phe
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 96 CGGGAGCATT TTATGACAAT AAAAGTGACAG CTGACAATTT TGCCTATAGA GTTAATTATG 842
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149	TTATTAAAAT	AACCAGCTA	CAATAACACT	ATCGGTCTAT	CTGACAGTT	TTCCCCCAGG	4022
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152	AAAGAGCATG	TTAGAGCTA	CAAATGCATA	AGCAAGACTG	AGCAGCATT	TAATTAAATT	4202

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 154 AAAAAAAA AAAA 4276
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 157 (i) SEQUENCE CHARACTERISTICS:
 158 (A) LENGTH: 2689 base pairs
 159 (B) TYPE: nucleic acid
 160 (C) STRANDEDNESS: double
 161 (D) TOPOLOGY: linear
 162 (ii) MOLECULE TYPE: cDNA
 163 (vi) ORIGINAL SOURCE:
 164 (A) ORGANISM: human
 165 (G) CELL TYPE: leukocyte
 166 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
 167 GTTGGAGGTT CTGGGGCGCA GAACCGCTAC TGCTGCTTCG GTCTCTCCTT GGGAAAAAAT 60
 168 AAAATTTGAA CCTTTGGAG CTGTGTGCTA AATCTTCAGT GGGACA ATG GGT TCA 115
 169 Met Gly Ser
 170 1
 171 GAC AAA AGA GTG AGT AGA ACA GAG CGT AGT GGA AGA TAC GGT TCC ATC 163
 172 Asp Lys Arg Val Ser Arg Thr Glu Arg Ser Gly Arg Tyr Gly Ser Ile
 173 5 10 15
 174 ATA GAC AGG GAT GAC CGT GAT GAG CGT GAA TCC CGA AGC AGG CGG AGG 211
 175 Ile Asp Arg Asp Asp Arg Asp Glu Arg Ser Arg Ser Arg Arg Arg
 176 20 25 30 35
 177 GAC TCA GAT TAC AAA AGA TCT AGT GAT GAT CGG AGG GGT GAT AGA TAT 259
 178 Asp Ser Asp Tyr Lys Arg Ser Ser Asp Asp Arg Arg Gly Asp Arg Tyr
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 181 Asp Asp Tyr Arg Asp Tyr Asp Ser Pro Glu Arg Glu Arg Glu Arg Arg
 182 55 60 65
 183 AAC AGT GAC CGA TCC GAA GAT GGC TAC CAT TCA GAT GGT GAC TAT GGT 355
 184 Asn Ser Asp Arg Ser Glu Asp Gly Tyr His Ser Asp Gly Asp Tyr Gly
 185 70 75 80
 186 GAG CAC GAC TAT AGG CAT GAC ATC AGT GAC GAG AGG GAG AGC AAG ACC 403
 187 Glu His Asp Tyr Arg His Asp Ile Ser Asp Glu Arg Glu Ser Lys Thr
 188 85 90 95
 189 ATC ATG CTG CGC GGC CTT CCC ATC ACC ATC ACA GAG AGC GAT ATT CGA 451
 190 Ile Met Leu Arg Gly Leu Pro Ile Thr Ile Thr Glu Ser Asp Ile Arg
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 192 GAA ATG ATG GAG TCC TTC GAA GGC CCT CAG CCT GCG GAT GTG AGG CTG 499
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 200 TGTTAGCATC TGAGGAACCTT TTTTAAACTT TGTTTTAGGG ACTTTTTTTT CCTTAGGTAA 725
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234	(2) INFORMATION FOR SEQ ID NO:3:						
235	(i) SEQUENCE CHARACTERISTICS:						
236	(A) LENGTH: 2981 base pairs						
237	(B) TYPE: nucleic acid						
238	(C) STRANDEDNESS: double						
239	(D) TOPOLOGY: linear						
240	(ii) MOLECULE TYPE: cDNA						
241	(vi) ORIGINAL SOURCE:						
242	(A) ORGANISM: human						
243	(G) CELL TYPE: leukocyte						
244	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:						
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/090,672B

DATE: 03/22/2000
TIME: 23:32:13

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Line	Error	Original Text
23	Wrong Classification	(C) CLASSIFICATION: 435

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